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PENSOFT

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A new tribe, genus, and species of freshwater mussel from the Changjiang River Basin in China (Bivalvia, Unionidae, Unioninae)

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https://zoobank.org/219F8CF1-F488-4B0C-9C65-F8FD98331040

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Abstract

A new tribe, genus, and species of freshwater mussels, Globunionini Dai, Chen, Huang & Wu, **tribe nov.** and *Globunio mirificus* Chen, Dai, Huang & Wu, **gen. et sp. nov.**, is described from the Changjiang River Basin in China based on comparative morphology and molecular phylogeny. The species presence of a special small-sized and elongated globular, which distinguishes it from all other tribes. The discovery increases the diversity of freshwater mussels in the Changjiang River Basin.

Key Words

Biodiversity, molluscs, phylogeny, taxonomy

Introduction

Freshwater mussels (Mollusca: Bivalvia: Unionida) play an important role in freshwater ecosystems (Graf and Cummings 2007; Huang et al. 2019) and are one of the most threatened freshwater organisms globally (Vaughn 2018; Lopes-Lima et al. 2020; Böhm et al. 2021). China is one of the regions with the highest species diversity of freshwater mussels in the world, with about 100 accepted species recorded and new taxa continuing to be discovered (Heude 1875, 1877a, 1877b, 1878, 1879, 1880a, 1880b, 1881, 1883, 1885; Simpson 1900; He and Zhuang 2013; Graf and Cummings 2021; Guo 2022; Liu et al. 2022; Wu et al. 2022a, 2022b; Chen et al. 2023; Dai et al. 2023, 2024a, 2024b, 2024c, 2024d). The freshwater mussels in China are mainly concentrated in the Changjiang River Basin (Yangtze), with about 70 accepted species recorded (Heude 1875, 1877a, 1877b, 1878, 1879, 1880a, 1880b, 1881, 1883, 1885; Simpson 1900; He and Zhuang 2013; Graf and Cummings 2021; Guo 2022; Chen et al. 2023; Dai et al. 2024a, 2024b). Even in the well-studied middle and lower reaches of the Changjiang River, new freshwater mussels have been continuously discovered in recent years, demonstrating the extremely high diversity in the region (Guo 2022; Chen et al. 2023; Dai et al. 2023, 2024a, 2024b; Wu et al. 2024).

During the surveys in 2022, we discovered a group of freshwater mussel specimens with the special small-sized and elongated-globular shell that did not resemble any known species and were challenging to place in any genus or tribe. Based on a combination of morphology and molecular phylogeny, we describe it as a new tribe, genus, and species of subfamily Unioninae Rafinesque, 1820. The discovery improved the diversity of freshwater mussels in the Changjiang River Basin and showed that even in the central city, there are still yet-to-be-described species of freshwater mussels that exist.

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Materials and methods

Materials preparation

Specimens were collected from Jiangxi, China, in 2022. Living specimens were initially frozen at -20 °C for 24 hours and subsequently thawed at room temperature for 2 hours to facilitate the extraction of soft parts. The soft parts were then fixed in 95% ethanol. Empty shells were cleaned, dried, and preserved at room temperature. Photographs were taken by camera and edited in Adobe Photoshop CC 2015 (Adobe, San Jose, US). Maps were made in ArcGIS Pro (Esri, Redlands, US).

DNA extraction, sequencing, and mitogenome assembly

Genomic DNA was extracted from muscle preserved in 95% ethanol using a TIANamp Marine Animals DNA Kit (Tiangen Biotech, China). The quality and concentration of the DNA were checked on 1% agarose gel electrophoresis and NanoDrop 2000 (Thermo Scientific, USA). The qualified genomic DNA sample was sent to Novogene (Beijing, China). Two datasets were used for phylogenetic analyses: the partial cytochrome c oxidase subunit 1 (*COI*) sequences and the mitochondrial genomes. The polymerase chain reaction (PCR) systems, conditions, and primer pairs of *COI* are followed by Chen et al. (2023). After quality controls, the library was successfully prepared and sequenced in the Illumina NovaSeq 6000 platform, yielding 12 Gb of data, with 2 × 150 bp paired-end reads. After discarding low-quality reads, clean reads were obtained and assembled de novo using CLC Genomic Workbench v. 12.0 (https://digitalinsights.qiagen.com). Contigs identified as mitogenome sequences were inspected manually for overlap at the beginning and end, resulting in a circular mitogenome. Geneious v. 11.0 (https://www.geneious.com) (Kearse et al. 2012) was used to check the complete mitogenome and analyze nucleotide composition. Strand asymmetry was calculated using the formulas: GC skew = (G−C)/(G+C) and AT skew = (A−T)/(A+T). The initial annotation of the mitogenome was carried out using the MITOS web server (http://mitos.bioinf.uni-leipzig.de/index.py) (Bernt et al. 2013). ARWEN (http://130.235.244.92/ARWEN) (Laslett and Canback 2008) was also used to identify the locations of all tRNA genes. The annotations of two rRNA genes were further refined based on the positions of neighboring genes. PCGs were initially identified using the Open Reading Frame Finder (ORF Finder) implemented on the NCBI website (http://www.ncbi.nlm.nih.gov/orffinder) and BLAST searches (http://blast.ncbi.nlm.nih.gov).

Alignments, partitioning strategies

The *COI* dataset consists of 51 sequences of the family Unionidae and two outgroup taxa (Table 1). The mitochondrial genome dataset consists of 81 sequences (including 12 PCGs (excluding ATP8) and two rRNA genes) of the family Unionidae and nine outgroup taxa (Table 2). The *COI* sequences were aligned using MEGA

Table 1. GenBank accession numbers of the *COI* sequences used in this study.

Species	Locality	Accession number	References
Unioninae Rafinesque, 1820			
Globunio mirificus gen. et sp. nov. 1	Honggutan, Nanchang, Jiangxi, China	PV368604	This study
Globunio mirificus gen. et sp. nov. 2	Honggutan, Nanchang, Jiangxi, China	PV368605	This study
Globunio mirificus gen. et sp. nov. 3	Honggutan, Nanchang, Jiangxi, China	PV368606	This study
Globunio mirificus gen. et sp. nov. 4	Honggutan, Nanchang, Jiangxi, China	PV368607	This study
Globunio mirificus gen. et sp. nov. 5	Honggutan, Nanchang, Jiangxi, China	PV368608	This study
Globunio mirificus gen. et sp. nov. 6	Honggutan, Nanchang, Jiangxi, China	PV368609	This study
Globunio mirificus gen. et sp. nov. 7	Honggutan, Nanchang, Jiangxi, China	PV368610	This study
Globunio mirificus gen. et sp. nov. 8	Honggutan, Nanchang, Jiangxi, China	PV368611	This study
Globunio mirificus gen. et sp. nov. 9	Honggutan, Nanchang, Jiangxi, China	PV368612	This study
Diaurora aurorea (Heude, 1883)	Ji'an, Jiangxi, China	OQ829360*	Chen et al. 2023
Acuticosta chinensis (Lea, 1868)	Jiangxi, China	MG462921	Huang et al. 2019
Schistodesmus lampreyanus (Baird & Adams, 1867)	Jiangxi, China	MG463037	Huang et al. 2019
Schistodesmus spinosus (Simpson, 1900)	Jiangxi, China	MG463046	Huang et al. 2019
Schistodesmus sp.	Hunan, China	MG463043	Huang et al. 2019
Unio pictorum (Linnaeus, 1758)	Europe	KC429109	Sharma et al. 2013
Unio crassus Philipsson, 1788	Poland	KY290446	Burzynski et al. 2017
Tchangsinaia piscicula (Heude, 1874)	Jiangxi, China	MG462977	Huang et al. 2019
Cuneopsis celtiformis (Heude, 1874)	Jiangxi, China	MG462964	Huang et al. 2019
Cuneopsis heudei (Heude, 1874)	Jiangxi, China	MG462970	Huang et al. 2019
Aculamprotula fibrosa (Heude, 1877)	Jiangxi, China	MG462909	Huang et al. 2019
Nodularia douglasiae (Gray, 1833)	China	KX822653	Lopes-Lima et al. 2017
Nodularia breviconcha Lee, Kim, Bogan & Kondo, 2020	South Korea	MT020662	Lopes-Lima et al. 2020

Species	Locality	Accession number	References
Inversiunio yanagawensis (Kondo, 1982)	Japan	MT020654	Lopes-Lima et al. 2020
Inversiunio reinianus (Kobelt, 1879)	Japan	MT020657	Lopes-Lima et al. 2020
Pseudocuneopsis sichuanensis Huang, Dai, Chen & Wu, 2022	Sichuan, China	MZ540966	Wu et al. 2022b
Pseudocuneopsis capitata (Heude, 1874)	Anhui, China	NC042469	Wu et al. 2019
Alasmidonta marginata Say, 1818	U.S.	AF156502	Graf & O'Foighil 2000
Lasmigona compressa (Lea, 1829)	U.S.	AF156503	Graf & O'Foighil 2020
Anodonta anatina (Linnaeus, 1758)	Russia	KX822632	Lopes-Lima et al. 2017
Pseudanodonta complanata (Rossmässler, 1835)	Ukraine	KX822661	Lopes-Lima et al. 2017
Lanceolaria gladiola (Heude, 1877)	Jiangxi, China	KY067441	Unpublished
Lanceolaria oxyrhyncha (Martens, 1861)	Japan	MT020648	Lopes-Lima et al. 2020
Cristaria plicata (Leach, 1814)	Jiangxi, China	MG462956	Huang et al. 2019
Lepidodesma languilati (Heude, 1874)	Jiangxi, China	MG463015	Huang et al. 2019
Sinanodonta woodiana (Lea, 1834)	China	KX822668	Lopes-Lima et al. 2017
Beringiana beringiana (Middendorff, 1851)	Japan	MT020557	Lopes-Lima et al. 2020
*Plethol*ophus *tenuis* (Gray, 1833)	Vietnam	KX822658	Lopes-Lima et al. 2016
Anemina arcaeformis (Heude, 1877)	Jiangxi, China	MG462936	Huang et al. 2019
Amuranodonta kijaensis Moskvicheva, 1973	Russia	MK574204	Bolotov et al. 2020
Parreysiinae Henderson, 1935			
Coelatura aegyptiaca (Cailliaud, 1823)	Egypt	KJ081162	Graf et al. 2014
Indonaia andersoniana (Nevill, 1877)	Myanmar	MF352275	Bolotov et al. 2017
Parreysia nagpoorensis (Lea, 1860)	India	JQ861229	Unpublished
Gonideinae Ortmann, 1916			
Pronodularia japanensis (Lea, 1859)	Japan	LC505454	Fukata and ligo 2020
Lamprotula leaii (Gray, 1833)	Jiangxi, China	MG462996	Huang et al. 2019
Ambleminae Rafinesque, 1820			
Lampsilis siliquoidea (Barnes, 1823)	U.S.	MH560773	Unpublished
Quadrula quadrula (Rafinesque, 1820)	U.S.	HM230409	Unpublished
Margaritiferidae Henderson, 1929			
Margaritifera dahurica (Middendorff, 1850)	Russia	KJ161516	Bolotov et al. 2015
Gibbosula rochechouartii (Heude, 1875)	Jiangxi, China	MG463022	Huang et al. 2019

X (Kumar et al. 2018) and checked manually. MUSCLE (Edgar 2004) was used for codon alignment of all PCGs implemented in MEGA X (Kumar et al. 2018). MAFFT (Katoh et al. 2019) with the Q-INS-i algorithm was used for the alignment of ribosomal genes (12S and 16S rRNAs). Gblocks (Castresana 2000) were used to exclude ambiguous regions from the alignment of each gene. PartitionFinder (Lanfear et al. 2017) was used to determine the best-fit partitioning schemes and substitution models under greedy search. Predefined data blocks for partitioning scheme searches were designated by gene region (rRNA gene) or codon position (PCG). Branch lengths were allowed to be unlinked, and model selection and partitioning schemes were determined using the AICc method (Table 3).

Phylogenetic analyses

ML analyses were performed in IQ-TREE v. 1.6.12 (Minh et al. 2013) using the Ultrafast bootstrap approach (Minh et al. 2013) with 10,000 iterations. Bayesian inference (BI) analysis was conducted in MrBayes v. 3.2.6 (Ronquist et al. 2012). Four simultaneous runs with four independent Markov Chain Monte Carlo (MCMC) were implemented for 10 million generations, and trees were sampled every 10,000 generations with a burn-in of 25%. The convergence was checked with the average standard deviation of split frequencies < 0.01 and the potential scale reduction factor (PSRF) ~ 1. Trees were visualized in FigTree v.1.4.3 (http://tree.bio.ed.ac.uk/software/figtree/).

Abbreviations

NCU_XPWU: Laboratory of Xiao-Ping Wu, Nanchang University (Nanchang, Jiangxi, China).

Results

COI phylogeny

The alignment of the *COI* gene had lengths of 606 characters. Within these alignments, 260 sites were variable, and 236 sites were parsimony informative. The maximum likelihood and Bayesian analyses produced consistent phylogenies (Figs 1, 2). Although a single gene marker cannot effectively address inter tribes relationships in the subfamily Unioninae, the new species formed an independent branch that does not belong to any tribe. Its systematic position needs further verification through mitochondrial genome phylogenetic analysis.

Table 2. GenBank accession numbers of the mitochondrial genome sequences used in this study.

Species	Accession number
Unioninae Rafinesque, 1820	
Globunio mirificus gen. et sp. nov.	PV394654
Tchangsinaia pisciculus (Heude, 1874)	NC026306
Cuneopsis heudei (Heude, 1874)	NC042471
Cuneopsis rufescens (Heude, 1874)	MZ571512
Cuneopsis celtiformis (Heude, 1874)	MW464617
Cuneopsis demangei Haas, 1929	MZ571513
Pseudocuneopsis capitata (Heude, 1874)	NC042469
Pseudocuneopsis capitata (Heude, 1874)	MZ571517
Pseudocuneposis sichuanensis Huang, Dai, Chen & Wu, 2022	MZ571510
Pseudocuneopsis yemaoi Dai, Chen, Huang & Wu, 2024	OR392755
Pseudocuneopsis yangshuoensis Wu & Liu, 2023	OR392756
Schistodesmus lampreyanus (Baird & Adams, 1867)	NC042470
Schistodesmus spinosus (Simpson, 1900)	MZ571511
Unio crassus Philipsson, 1788	KY290446
Unio delphinus Spengler, 1793	KT326917
Unio pictorum (Linnaeus,1758)	NC015310
Unio tumidus Philipsson, 1788	KY021076
Nodularia breviconcha Lee, Kim, Bogan & Kondo	MT955592
Nodularia douglasiae (Griffith & Pidgeon, 1833)	NC026111
Nodularia fusiformans Wu & Liu, 2024	MT764726
Nodularia nuxpersicae (Dunker, 1848)	OR888962
Nodularia nuxpersicae (Dunker, 1848)	OR888961
Aculamprotula coreana (Martens, 1886)	NC026035
Aculamprotula polysticta (Heude, 1877)	MK728823
Aculamprotula scripta (Heude, 1875)	MF991456
Aculamprotula tientsinensis (Crosse & Debeaux, 1863)	NC029210
Aculamprotula tortuosa (Lea, 1865)	NC021404
Acuticosta chinensis (Lea, 1868)	MF687347
Anodonta anatina (Linnaeus, 1758)	NC022803
Anodonta cygnea (Linnaeus, 1758)	NC036488
Sinanodonta lucida (Heude, 1877)	NC026673
Sinanodonta woodiana (Lea, 1834)	HQ283346
Cristaria plicata (Leach, 1814)	NC012716
Anemina arcaeformis (Heude, 1877)	NC026674
Anemina euscaphys (Heude, 1879)	NC026792
Utterbackia imbecillis (Say, 1829)	NC015479
Utterbackia peninsularis Bogan & Hoeh, 1995	HM856636
Pyganodon grandis (Say, 1829)	NC013661
Lasmigona compressa (Lea, 1829)	NC015481
Lanceolaria gladiola (Heude, 1877)	KY067441
Lanceolaria grayii (Gray, 1833)	NC026686
Lanceolaria lanceolata (Lea, 1856)	NC023955
Lepidodesma languilati (Heude, 1874)	NC029491
Gonideinae Ortmann, 1916	
Sinosolenaia carinata (Heude, 1877)	NC023250
Sinosolenaia oleivora (Heude, 1877)	NC022701
Ptychorhynchus pfisteri (Heude, 1874)	KY067440
Parvasolenaia rivularis (Heude, 1877)	KX966393
Inversidens rentianensis Wu & Wu, 2021	OR823224
Postolata guangxiensis Dai, Huang, Guo & Wu, 2023	OP009366
Microcondylaea bonellii (Férussac, 1827)	NC044111
Monodontina vondembuschiana (Lea, 1840)	NC044112
Pilsbryoconcha exilis (Lea, 1838)	NC044124
Lamprotula gottschei-Schistodesmus.sp	NC023806
Lamprotula leaii (Griffith & Pidgeon, 1833)	NC023346
Lamprotula caveata (Heude, 1877)	NC030336
Pronodularia japanensis (Lea, 1859)	AB055625
Potomida littoralis (Cuvier, 1798)	NC030073
Sinohyriopsis cumingii (Lea, 1852)	NC011763
Sinohyriopsis schlegelii (Martens, 1861)	NC015110
Chamberlainia hainesiana (Lea, 1856)	NC044110
Lens contradens (Lea, 1838)	MW242812
Physunio superbus (Lea, 1843)	MW242814
Hyriopsis bialata Simpson, 1900	MW242816
Rectidens sumatrensis (Dunker, 1852)	MW242818
Lampsilis powellii (Lea, 1852)	NC037720

Species	Accession number
Lampsilis siliquoidea (Barnes, 1823)	NC037721
Lampsilis cardium Rafinesque, 1820	BK010478
Lampsilis ornata (Conrad, 1835)	NC005335
Venustaconcha ellipsiformis (Conrad, 1836)	FJ809753
Leaunio lienosus (Conrad, 1834)	BK010479
Potamilus leptodon (Rafinesque, 1820)	NC028522
Potamilus alatus (Say, 1817)	KU559010
Toxolasma parvum (Barnes, 1823)	NC015483
Popenaias popeii (Lea, 1857)	NC050058
Amblema plicata (Say, 1817)	NC050056
Elliptio complanata (Lightfoot, 1786)	BK010477
Pleurobema oviforme (Conrad, 1834)	NC050057
Quadrula quadrula (Rafinesque, 1820)	NC013658
Uniomerus tetralasmus (Say, 1831)	BK010480
Margaritiferidae Henderson, 1929	
Margaritifera dahurica (Middendorff, 1850)	NC023942
Margaritifera margaritifera (Linnaeus, 1758)	MK421958
Margaritifera falcata (Gould, 1850)	NC015476
Pseudunio marocanus (Pallary, 1918)	KY131953
Cumberlandia monodonta (Say, 1829)	KU873123
Gibbosula rochechouartii (Heude, 1875)	KX378172
Hyriidae Swainson, 1840	
Echyridella menziesii (Gray, 1843)	KU873121
Iridinidae Swainson, 1840	
Mutela dubia (Gmelin, 1791)	KU873120
Mycetopodidae Gray, 1840	
Anodontites trapesialis (Lamarck, 1819)	KU873119

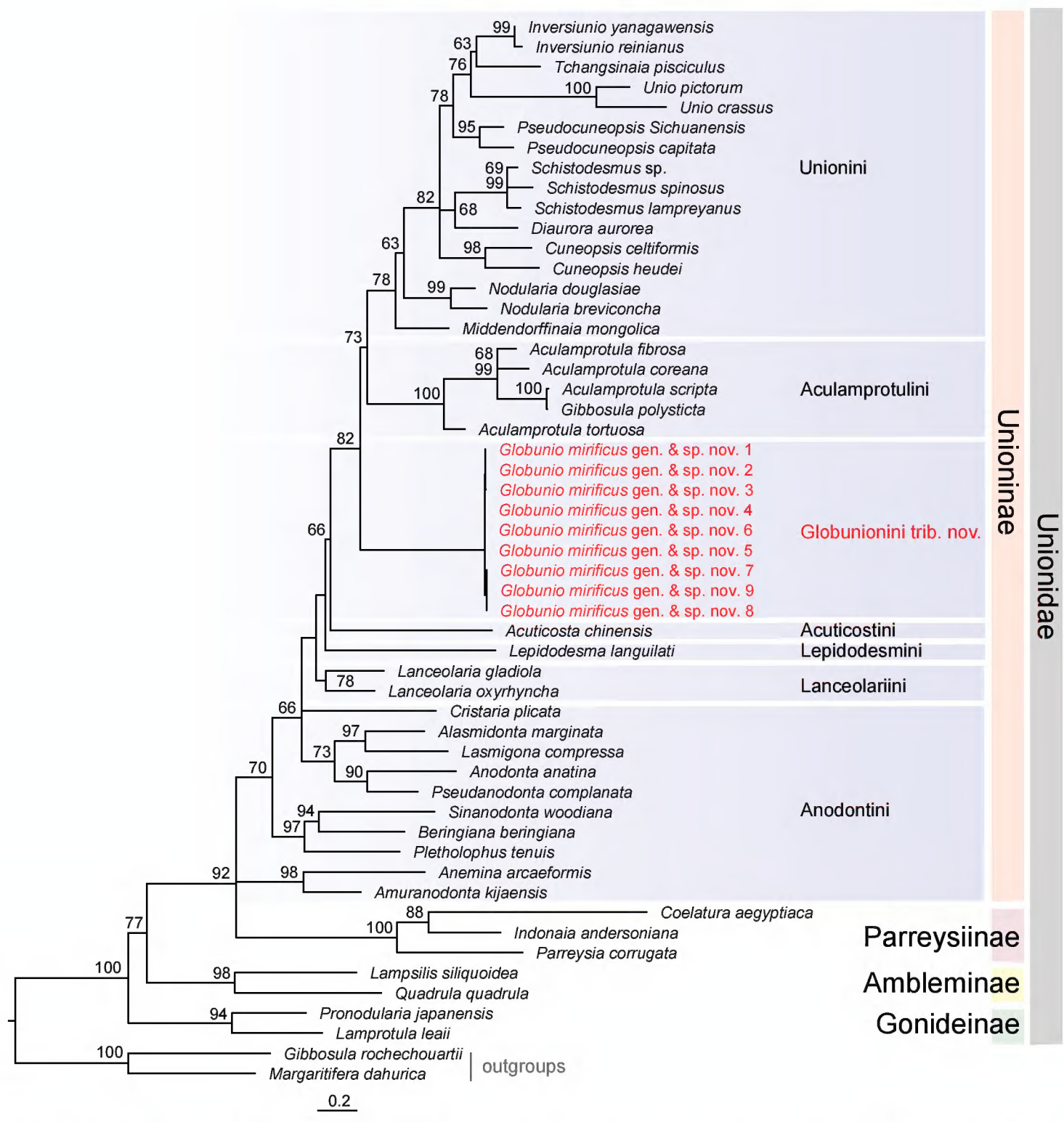

Figure 1. Maximum likelihood tree inferred from *COI* gene sequences. Bootstrap supports are shown on the left of nodes on the tree if greater than 50%.

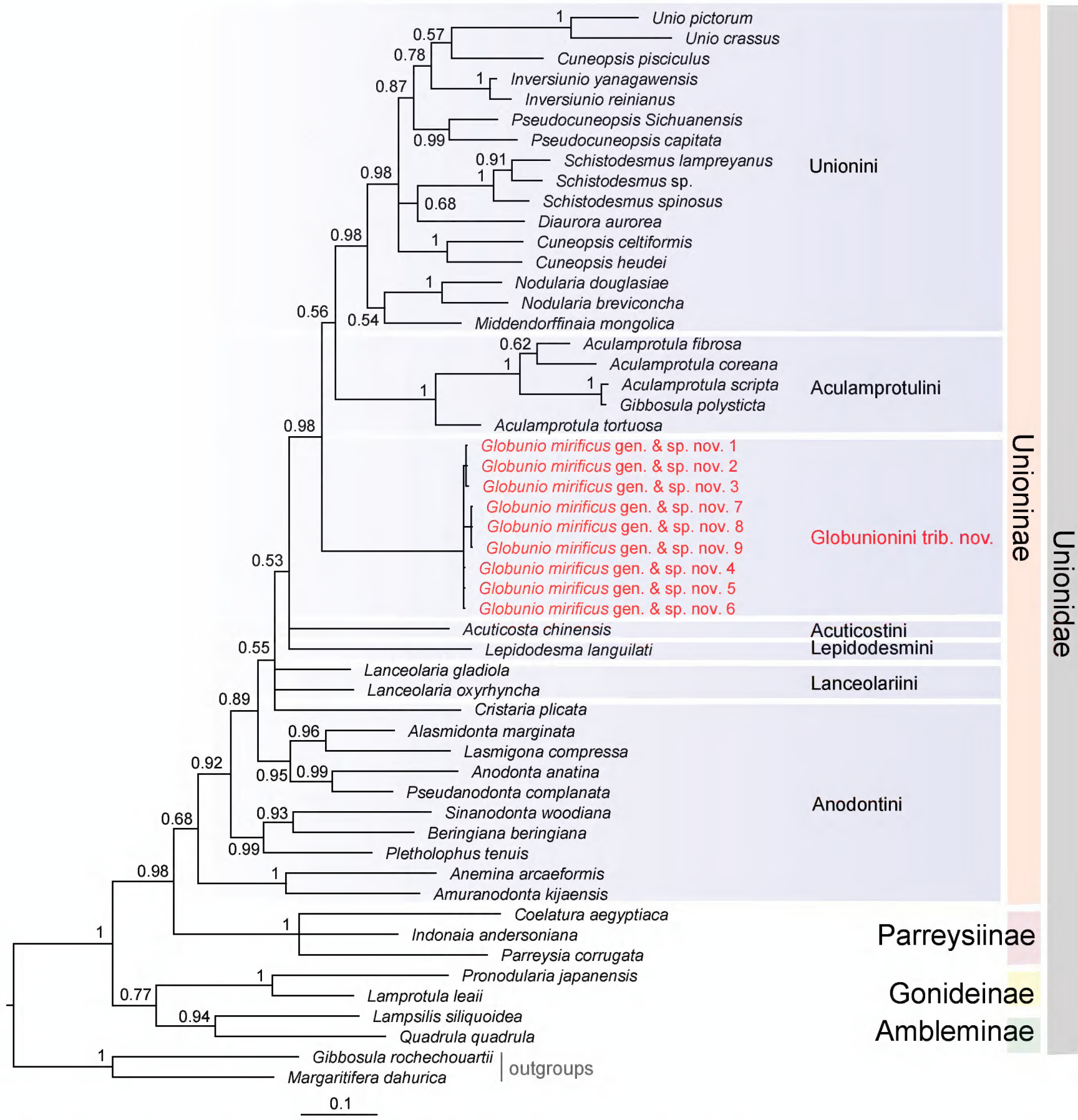

Figure 2. Bayesian inference tree inferred from *COI* gene sequences. Posterior probabilities are shown on the left of nodes on the tree if greater than 50%.

Table 3. Partitioning strategies for the mitogenome dataset (from PartitionFinder2) according to AICc.

Subset	Best Model	Partition scheme
1	GTR+I+G	COX1 codon1, ATP6 codon1, ND4 codon1, ND3 codon1, ND5 codon1, ND4L codon1, CO3 codon1
2	GTR+I+G	ND5 codon2, ND3 codon2, ND4L codon2, COX1 codon2, CO3 codon2, ND4 codon2, ATP6 codon2
3	GTR+I+G	CO2 codon3, ND4L codon3, ND3 codon3, ATP6 codon3, ND4 codon3, ND5 codon3, CO3 codon3, COX1 codon3
4	SYM+I+G	ND1 codon1, CYTB codon1, CO2 codon2, CO2 codon1
5	GTR+I+G	ND1 codon2, ND6 codon2, ND2 codon2, CYTB codon2
6	GTR+G	ND1 codon3, ND6 codon3, CYTB codon3, ND2 codon3
7	GTR+I+G	16S, 12S, ND2 codon1, ND6 codon1

Mitogenome characteristics

The length of the mitogenome is 16,240 bp. The maternal mitogenomes of the new species contain the 13 PCGs typically found in metazoan mitochondrial genomes, the type-specific F-orf described for all Unionida mitogenomes with the DUI system, 22 transfer RNA (tRNA), and two ribosomal RNA (rRNA) genes (Fig. 3A). Most genes were encoded on the light strand (L-strand), whereas 11 genes (COI, COII, COIII, ND3, ND4, ND4L, ND5, ATP6, ATP8, $tRNA^{Asp}$, and $tRNA^{His}$) were located on the heavy strand (H-strand). The location of the F-orf was between ND2 and $tRNA^{Glu}$, and the gene order of the mitogenomes was consistent with other Unioninae and Ambleminae species. The rrnS gene of it was located between $tRNA^{Arg}$ and $tRNA^{Lys}$, while the rrnL gene was located between $tRNA^{Tyr}$

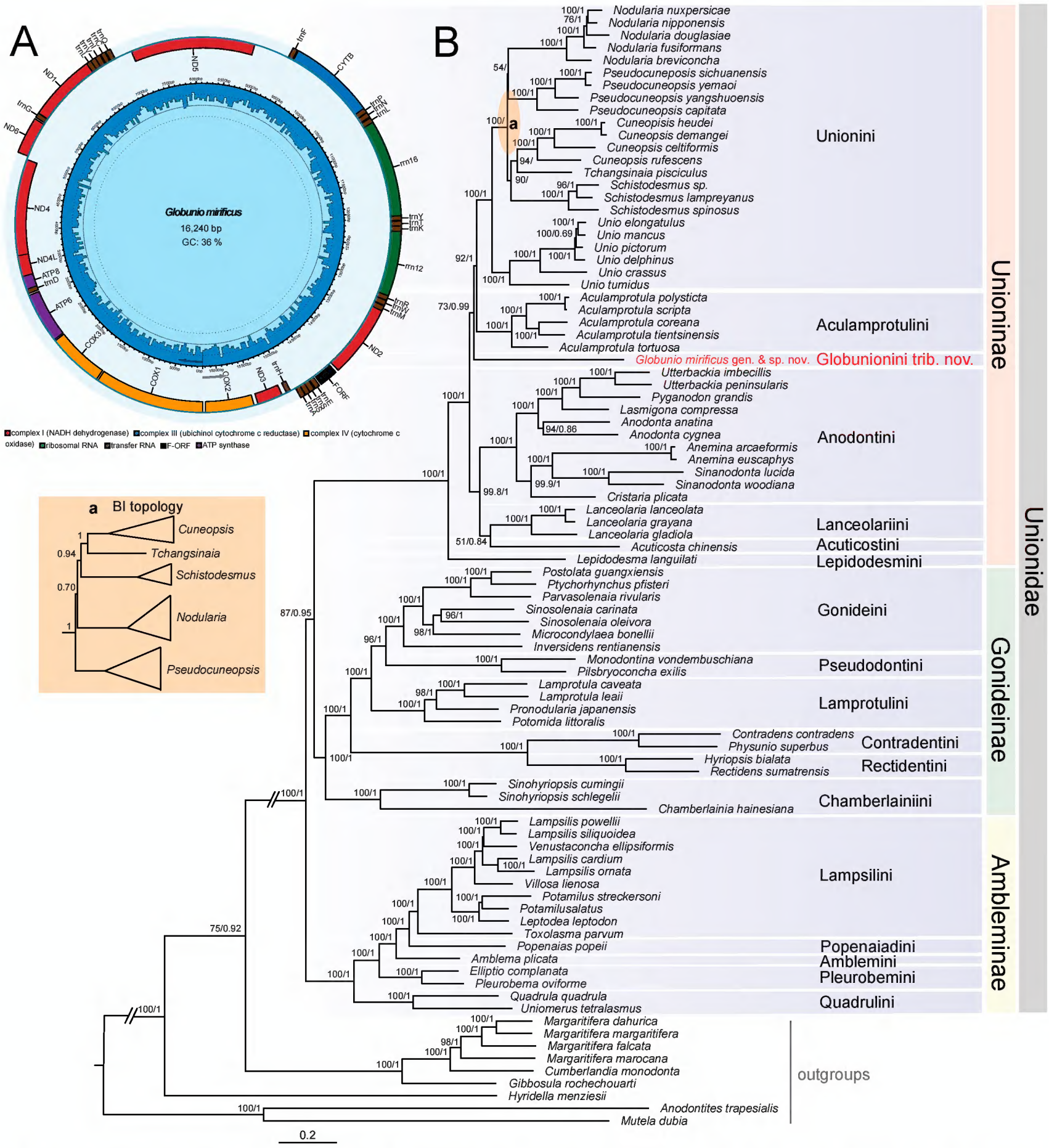

Figure 3. A. Gene map of the F-type mitochondrial genome of *Globunio mirificus* gen. et sp. nov.; **B.** Maximum likelihood and Bayesian inference tree inferred from mitochondrial genome sequences. Bootstrap supports/posterior probabilities are shown on the left/right of nodes on the tree if they are greater than 50%.

and $tRNA^{Leu}$. The overall base composition was A (25.7%), T (38.1%), C (12.2%), and G (24.0%), with the A + T content of 63.8%. Nucleotide asymmetry of the mitochondrial strands was assessed by AT skew and GC skew that were −0.19 and 0.33, respectively.

Mitochondrial phylogeny

The alignment of the mitogenomes had lengths of 11,547 characters. Within these alignments, 7,300 sites were variable, and 6,604 sites were parsimony informative. The maximum likelihood and Bayesian analyses produced largely consistent phylogenies (Fig. 3B). The new species formed an independent branch in the subfamily Unioninae and was sistered with the clade consisting of Unionini + Aculamprotulini with a relatively well support rate (BS/PP = 70/0.99).

Systematics

Family Unionidae Rafinesque, 1820
Subfamily Unioninae Rafinesque, 1820

Tribe Globunionini Dai, Chen, Huang & Wu, tribe nov.
https://zoobank.org/C3AC71B4-5393-4B57-B8C9-5D067E23B3E1

Type genus. *Globunio* Dai, Chen, Huang & Wu, 2024, gen. nov.

Diagnosis. Shell small-sized, elongated-globular, inflated, thick, solid; very wide, with some individuals even wider than height. Anterior extremely short, inflated, and round; posterior long and flat. Anterior margin rounded, dorsal margin straightened, and slope downward at an obtuse angle, usually covered in fine upward wrinkles; ventral margin weakly curved. Umbo inflated, under dorsal margin, almost at the very front of the shell, often eroded.

Vernacular name. 球蚌族 (qiú bàng zú).

Remarks. The new tribe has a special small, thick, and elongated-globular shell, which is completely dissimilar to all other tribes of the subfamily. Its independence was also supported by the molecular phylogeny.

Genus *Globunio* Dai, Chen, Huang & Wu, gen. nov.

https://zoobank.org/88F4B05A-65A8-49E6-A339-DAE71D4DC071

Type species. *Globunio mirificus* Chen, Dai, Huang & Wu, 2024, sp. nov.

Diagnosis. Same as the tribe.

Etymology. The species is made from the Latin g*lob* for globular, and unio for the unionid type genus.

Vernacular name. 球蚌属 (qiú bàng shǔ).

Globunio mirificus Chen, Dai, Huang & Wu, sp. nov.

https://zoobank.org/C2C368AA-A510-4FDC-B58C-C037009B42CB

Figs 4, 6C, D

Holotype. 24_NCU_XPWU_GM01, ♀, Honggutan District [红谷滩区], Nanchang City [南昌市], Jiangxi Province [江西省], China, 24.68146°N, 109.69794°E, leg. Zhong-Guang Chen & Yu-Ting Dai, September 2022.

Paratypes. n = 10, 24_NCU_XPWU_GM02, Honggutan District [红谷滩区], Nanchang City [南昌市], Jiangxi Province [江西省], China, 24.68146°N, 109.69794°E, leg. Zhong-Guang Chen, December 2021; 24_NCU_XPWU_GM03–11, other information same as holotype.

Diagnosis. Same as the tribe.

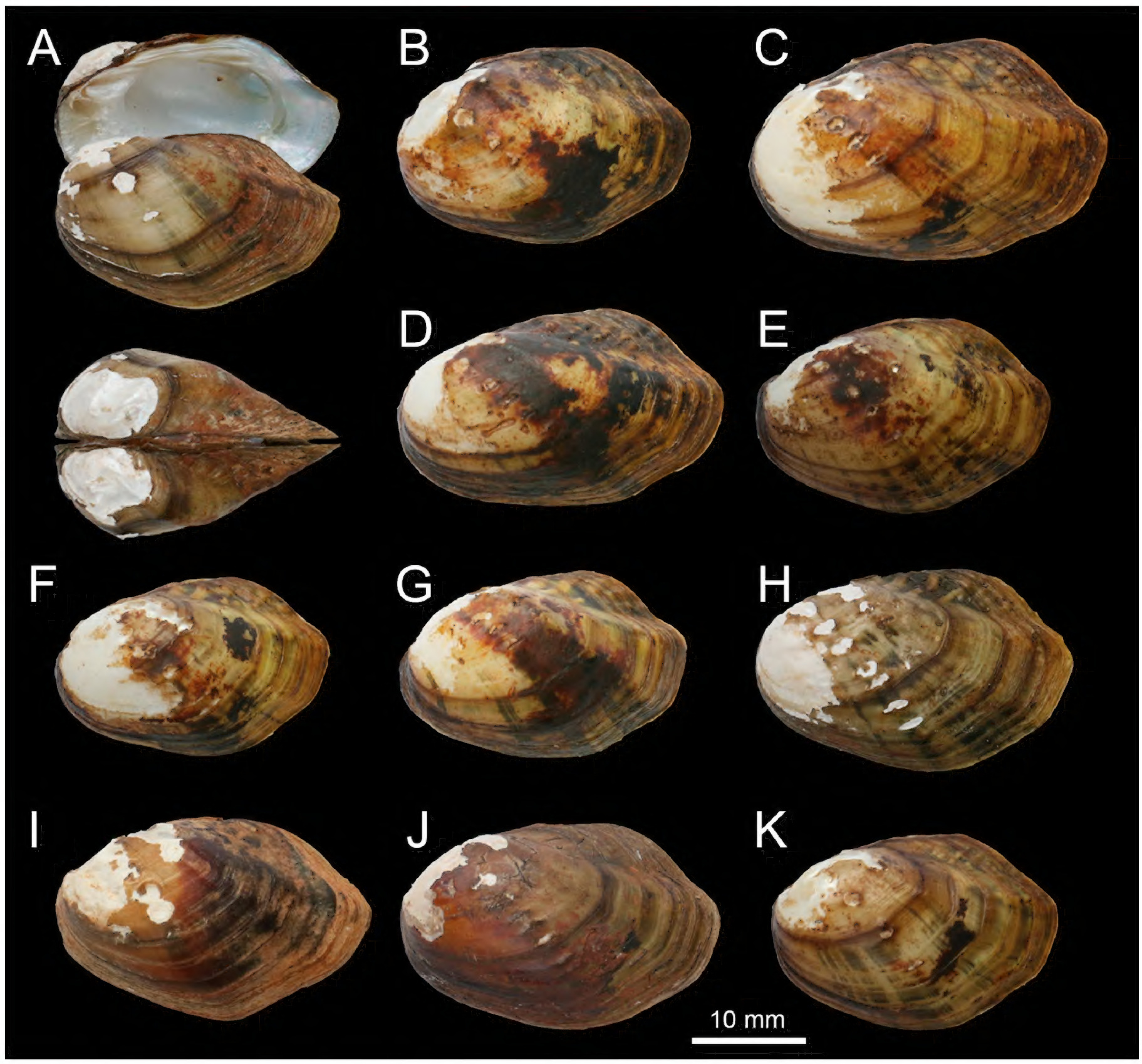

Figure 4. *Globunio mirificus* gen. et sp. nov. **A.** Holotype; **B–K.** Paratypes.

Description. Shell small-sized, elongated-globular, inflated, thick, solid. Anterior extremely short, inflated, and round; posterior long and flat. Anterior margin rounded, dorsal margin straightened, and slope downward at an obtuse angle, usually covered in fine upward wrinkles; ventral margin weakly curved. Umbo inflated, under dorsal margin, almost at the very front of the shell, often eroded. Central of shell with two rows of posterior dorsal spines (usually detached with only attachment marks), the anterior row longer and the posterior row shorter. Periostracum yellowish-green with olive-green rays and several thick growth lines. Hinge short and strong. Hinge developed. Left valve with two pseudocardinal teeth, anterior tooth small, triangular-shaped, posterior tooth well-developed, rectangular-shaped; right valve with a single well-developed, pyramidal pseudocardinal tooth. Both valves with two lateral teeth: left valve external weak, internal well-developed; right valve external well-developed, internal weak. Mantle attachment scars on the pallial line obvious. Anterior adductor muscle scars deep, samll; posterior adductor muscle scars shallow, orbicular-shaped. Umbo cavity open, deep. Nacre milky white.

Measurements. Shell length 15.07–32.37 mm, width 9.83–21.54 mm, height 13.06–19.30 mm.

Etymology. The species is named after the Latin *mirificus* for remarkable, referring to the remarkable shell morphology of this species.

Vernacular name. 奇异球蚌 (qí yì qiú bàng).

Distribution and ecology. Known from three localities of the Changjiang River Basin: the Ganjiang River at Nanchang, the Dongtinghu Lake at Yueyang, and the Qingyijiang River at Wuhu (Fig. 5). Living in the slow-flowing rivers and lakes with muddy and sandy substrates alongside dozens of other freshwater mussels (Fig. 6).

Discussion

Of all freshwater mussels of subfamily Unioninae, only partial species of Aculamprotulini have a somewhat similar elongated-globular shell with the new species. However, the new species has a much smaller (shell length < 35 mm), more expanded, and symmetric shell, while Aculamprotulini has a larger (shell length > 100 mm), flatter, and asymmetrical shell. A thorough examination of type specimens and more than 100 live animals of the new species has revealed that individuals over 15 mm frequently exhibit severe corrosion. This finding serves as a reliable indicator of the animals' advanced age, thereby confirming their status as adults rather than juveniles of other species. The new species is one of the smallest freshwater mussels in China.

The type locality of the new species was located in the central city of Nanchang, a region that has been extensively surveyed for freshwater mussels in China. However, due to the general lack of sensitivity amongst researchers to freshwater mussel classification, this species was overlooked for a considerable period. Its distribution in densely populated areas poses a significant threat to its survival. The preference of microhabitats with flowing and fine sediment, resulting in a very narrow distribution of the new species in the Ganjiang River. However, all the sediment at its type locality was completely excavated in 2023 for the construction of a water plant (Fig. 6B). Surveys conducted between 2023 and 2025, following the

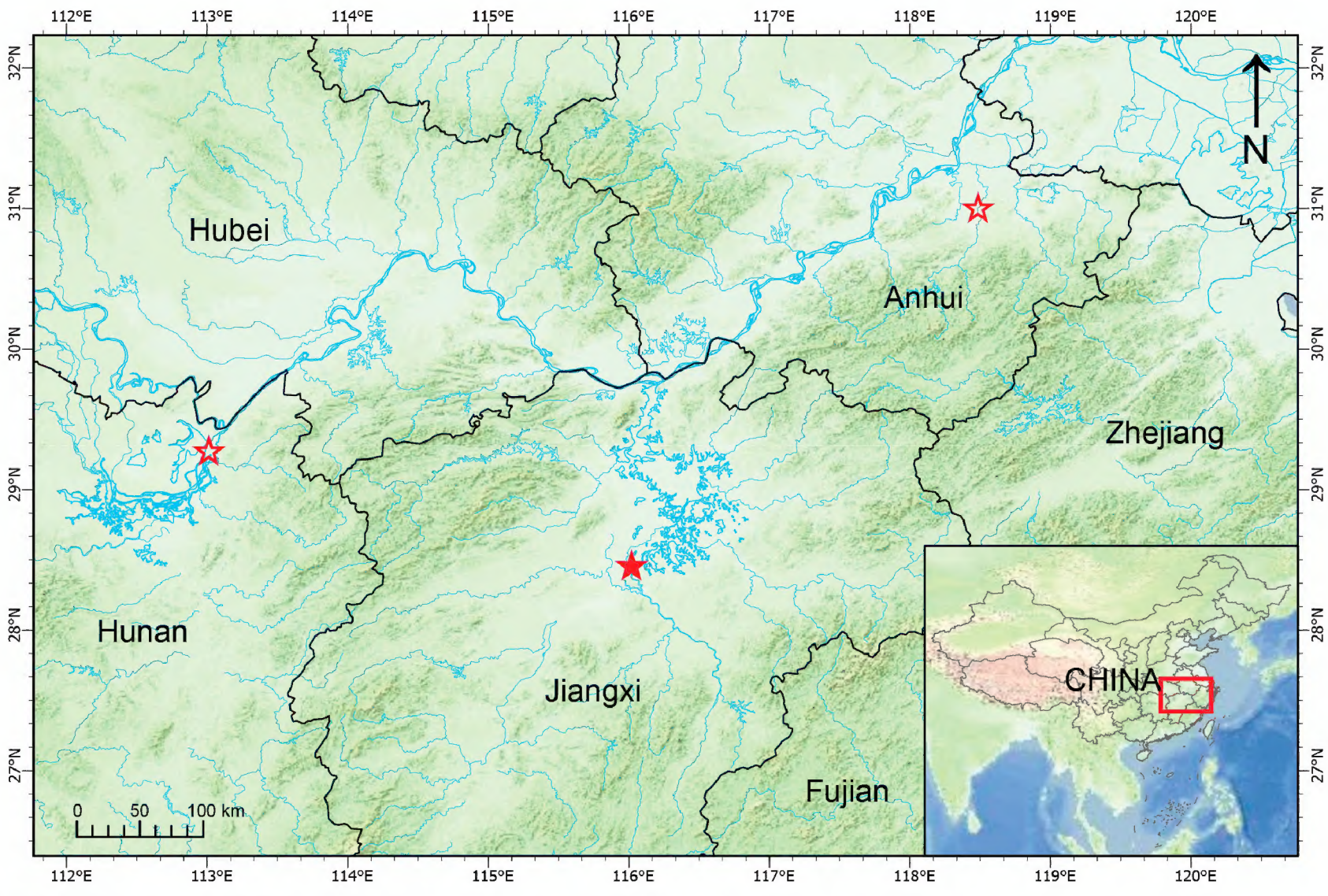

Figure 5. Distribution of *Globunio mirificus* gen. et sp. nov. Solid star: type locality; hollow stars: other localities.

Figure 6. Habitats and live animals of *Globunio mirificus* gen. et sp. nov. **A.** Type locality, Ganjiang River at Honggutan of Nanchang in 2022; **B.** Type locality, Ganjiang River at Honggutan of Nanchang in 2023; **C, D.** Live animals.

completion of the water plant, failed to recover any live animals. Furthermore, the construction of multiple dams (called the Ganfuweilyu Project) in the lower reaches of the Ganjiang River in 2024, resulting in the storage of water, has led to an increase in the average water level by 10 meters, thereby transforming the river into a static reservoir. This has led to concerns regarding the survival of new species that are dependent on flowing microhabitats. In addition to the type locality, the new species has also been discovered in Hunan and Anhui. The population size in Anhui is relatively large, but only empty shells have been found in Hunan. Protective measures such as artificial reproduction and ex situ conservation should be implemented for this species in order to save its declining population.

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